The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 10/539,725

Source: Pdf

Date Processed by STIC: 6/29/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER**
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED   **SUGGESTED CORRECTION**   **SERIAL NUMBER:** 10/539,725

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                         prevent "wrapping."

2 ___ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
      Numbering   use space characters, instead.

4 ___ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                         ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length   Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                         each n or Xaa can only represent a single residue. Please present the maximum number of each
                         residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                         previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                         the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                         Artificial or Unknown sequences.

7 ___ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         This sequence is intentionally skipped

                         Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
      (NEW RULES)   <210> sequence id number
                         <400> sequence id number
                         000

9 ___ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                         In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                         is Artificial Sequence

11 ___ Use of <220>   Sequence(s) _86_ missing the <220> "Feature" ~~and associated numeric identifiers and responses.~~
                         Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                         "Unknown." Please explain source of genetic material in <220> to <223> section. ————
                         (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                         listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

PCT

RAW SEQUENCE LISTING   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:07:59

Input Set : E:\05-06-06 1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

```
     3 <110> APPLICANT: greenovation Biotech GmbH
     5 <120> TITLE OF INVENTION: Improvements in or relating to protein production
     7 <130> FILE REFERENCE: Protein Production Method
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/539,725
C--> 11 <141> CURRENT FILING DATE: 2005-06-20
    11 <160> NUMBER OF SEQ ID NOS: 89
    13 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed
CPS. 1-6

ERRORED SEQUENCES

```
    15 <210> SEQ ID NO: 1
    16 <211> LENGTH: 36
    17 <212> TYPE: DNA
    18 <213> ORGANISM: Artificial Sequence
W--> 19 <220> FEATURE:        Pls insert mandatory <220> whenever
    19 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence MoB323     <221>, <222> or <223> is present.
    20 <400> SEQUENCE: 1
E--> 21 atactcgagg aagatgaact tttctgcctg tcttgg
    22 36        → Pls see item #10 on error summary sheet.
    24 <210> SEQ ID NO: 2
    25 <211> LENGTH: 26
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Artificial Sequence
W--> 28 <220> FEATURE:        same error
    28 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence MoB349
    29 <400> SEQUENCE: 2
E--> 30 ctgccatggg tgcagcctgg gaccac
    31 26        → See item #1 on error summary sheet.
    33 <210> SEQ ID NO: 3
    34 <211> LENGTH: 23
    35 <212> TYPE: DNA
    36 <213> ORGANISM: Artificial Sequence
W--> 37 <220> FEATURE:        same error
    37 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT(d)1
    38 <400> SEQUENCE: 3
E--> 39 gtngcngcng tngtngtnat ggc
    40 23        → same error
    42 <210> SEQ ID NO: 4     Pls explain "N" locations. Pls see
    43 <211> LENGTH: 27          error explanation
    44 <212> TYPE: DNA          on page 2.
    45 <213> ORGANISM: Artificial Sequence
W--> 46 <220> FEATURE:        same error
```

See item #11 on error summary sheet.

RAW SEQUENCE LISTING   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:07:59

Input Set : E:\05-06-06-1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

[handwritten: Same error see error explanation on pg. 7]

```
    46 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN(d)3
E-> 47 <400> SEQUENCE: 4
E-> 48 scyttrtang cngcnctgng gnacnco          [handwritten: Same error]
    49 27
    51 <210> SEQ ID NO: 5
    52 <211> LENGTH: 25
    53 <212> TYPE: DNA
    54 <213> ORGANISM: Artificial Sequence
W-> 55 <220> FEATURE:                          [handwritten: Same error]
    55 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN(d)2
    56 <400> SEQUENCE: 5
E-> 57 tayaaratng agncaytaya artgg
    58 25                                       [handwritten: See item #1 on error summary sheet]
    60 <210> SEQ ID NO: 6                       [handwritten: Same error]
    61 <211> LENGTH: 23
    62 <212> TYPE: DNA
    63 <213> ORGANISM: Artificial Sequence
W-> 64 <220> FEATURE:
    64 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN(d)4
    65 <400> SEQUENCE: 6
E-> 66 arttaytgyt traaraaytg ncc                [handwritten: Same error]
    67 23
    69 <210> SEQ ID NO: 7
    70 <211> LENGTH: 20
    71 <212> TYPE: DNA
    72 <213> ORGANISM: Artificial Sequence
W-> 78 <220> FEATURE:                          [handwritten: Same error]
    73 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACEG3
    74 <400> SEQUENCE: 7
E-> 75 gtccgtgtcc aataaaggag
    76 20
    78 <210> SEQ ID NO: 8
    79 <211> LENGTH: 21
    80 <212> TYPE: DNA
    81 <213> ORGANISM: Artificial Sequence     [handwritten: Same error]
W-> 82 <220> FEATURE:
    82 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACEG4
    83 <400> SEQUENCE: 8
E-> 84 gtcgggagag atttccatgt c
    85 21
    87 <210> SEQ ID NO: 9
    88 <211> LENGTH: 20
    89 <212> TYPE: DNA
    90 <213> ORGANISM: Artificial Sequence
W-> 91 <220> FEATURE:                          [handwritten: Same error]
    91 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACEG5
    92 <400> SEQUENCE: 9
E-> 93 ctaagatgac gacccttcgg
    94 20
```

[handwritten: See item #11 on error summary sheet]

SAME errors

```
     96 <210> SEQ ID NO: 10
     97 <211> LENGTH: 22
     98 <212> TYPE: DNA
     99 <213> ORGANISM: Artificial Sequence
W--> 100 <220> FEATURE:
     100 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACE6
E--> 101 <400> SEQUENCE: 10
E--> 102 catcctgaga aacaaaaagt gg
     103 22

    105 <210> SEQ ID NO: 11
    106 <211> LENGTH: 21
    107 <212> TYPE: DNA
    108 <213> ORGANISM: Artificial Sequence
W--> 109 <220> FEATURE:
    109 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACE7
E--> 110 <400> SEQUENCE: 11
E--> 111 agttacagac ttcaatgtac g
    112 21

    114 <210> SEQ ID NO: 12
    115 <211> LENGTH: 20
    116 <212> TYPE: DNA
    117 <213> ORGANISM: Artificial Sequence
W--> 118 <220> FEATURE:
    118 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 5RACE8
E--> 119 <400> SEQUENCE: 12
E--> 120 aatcaggacg gttgcaagcc
    121 20

    123 <210> SEQ ID NO: 13
    124 <211> LENGTH: 20
    125 <212> TYPE: DNA
    126 <213> ORGANISM: Artificial Sequence
W--> 127 <220> FEATURE:
    127 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 3RACEG1
E--> 128 <400> SEQUENCE: 13
E--> 129 ttatccgacc tgaagtttgc
    130 20

    132 <210> SEQ ID NO: 14
    133 <211> LENGTH: 20
    134 <212> TYPE: DNA
    135 <213> ORGANISM: Artificial Sequence
W--> 136 <220> FEATURE:
    136 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence 3RACEG2
E--> 137 <400> SEQUENCE: 14
E--> 138 gacctacaat tttggagagc
    139 20

    141 <210> SEQ ID NO: 15
    142 <211> LENGTH: 20
    143 <212> TYPE: DNA
    144 <213> ORGANISM: Artificial Sequence
```

Input Set : E:\05-06-06-1041WO.txt
Output Set : N:\CRF4\06292005\J539725.raw

√ SAME errors

```
W--> 145 <220> FEATURE:
    145 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT5F
E--> 146 <400> SEQUENCE: 15
E--> 147 tgggctttaa cacaactttt
    148 20
    150 <210> SEQ ID NO: 16
    151 <211> LENGTH: 19
    152 <212> TYPE: DNA
    153 <213> ORGANISM: Artificial Sequence
W--> 154 <220> FEATURE:
    154 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GTN6R
E--> 155 <400> SEQUENCE: 16
E--> 156 gccctaagct tgatccctg
    157 19
    159 <210> SEQ ID NO: 17
    160 <211> LENGTH: 21
    161 <212> TYPE: DNA
    162 <213> ORGANISM: Artificial Sequence
W--> 163 <220> FEATURE:
    163 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT21F
E--> 164 <400> SEQUENCE: 17
E--> 165 atggcagata tggctcgatt g
    166 21
    168 <210> SEQ ID NO: 18
    169 <211> LENGTH: 22
    170 <212> TYPE: DNA
    171 <213> ORGANISM: Artificial Sequence
W--> 172 <220> FEATURE:
    172 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNT15R
E--> 173 <400> SEQUENCE: 18
E--> 174 agtttctatg gtatctaact gc
    175 22
    177 <210> SEQ ID NO: 19
    178 <211> LENGTH: 21
    179 <212> TYPE: DNA
    180 <213> ORGANISM: Artificial Sequence
W--> 181 <220> FEATURE:
    181 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNTHT7
E--> 182 <400> SEQUENCE: 19
E--> 183 gagcatccaa gcttgacctg g
    184 21
    186 <210> SEQ ID NO: 20
    187 <211> LENGTH: 22
    188 <212> TYPE: DNA
    189 <213> ORGANISM: Artificial Sequence
W--> 190 <220> FEATURE:
    190 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer sequence GNTET7
E--> 191 <400> SEQUENCE: 20
E--> 192 gcaccgtgaa ttcttctagc tt
```

Input Set: E:\05-06-06 1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

```
193 22
780 <210> SEQ ID NO: 86
781 <211> LENGTH: 815
782 <212> TYPE: DNA
783 <213> ORGANISM: Artificial Sequence
784 <220> FEATURE:
784 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR product
785 <400> SEQUENCE: 86
786 gtccgcggt gatcccgttt tcatatcagt gtattatcat cagtgactgc atattgacac
787 60
788 caattctga tgattttta ttttttattt tttattttttt ttggtatggt tacatgcttt
789 120
790 tcagaggttt ctatgccgct gagtattttc ctgaatcgcg aggtgtgaca ggttatctgc
791 180
792 gccgtccacc caatatttta tgatgagtcg atgattcgtg agactaatct agcttaacct
793 240
794 tttcttact ggcaagtcaa aattgagttt aaaatatttc agtatcctgt tagtaatttc
795 300
796 agacacatgt attctatgtc tcatactctt tacgtgaaag ttcaactgac ttatatttg
797 360
798 tcgtttttct gtagatcact gtttagcgc atacaaagac aattgtctaa atatttttaa
799 420
800 agaaggtgat attttattat aagatagaag tcaatatgtt tttttgttat gcacatgact
801 480
802 tgaataaaat aaattttttt gttagattta aatacttttt gaattatagc tttgttgaaa
803 540
804 ttaaggaatt tatattcata agaagctact cgaacaaatt tacaaagaga acatttgata
805 600
806 agtaaaagta attaaaagtt tttttaatt taaaaagatt aattttatt aataagaaga
807 660
808 acttggaaag ttagaaaaat atttaacttt aaaaattaag aaaacaaggc aaaactttaa
809 720
810 ttacaaata cttaatgtag attaattttc ttattatata ttagcacaaa ttatcattat
811 780
812 gtgatatttt atgttattgt tacgtagagc tcaaa
813 815
833 <210> SEQ ID NO: 89
834 <211> LENGTH: 882
835 <212> TYPE: DNA
836 <213> ORGANISM: Artificial Sequence
837 <220> FEATURE:
837 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR product
838 <400> SEQUENCE: 89
839 cgcgttaact ctctctatct ctctctgtgt tgcgtttgat caggggtttt agggtttggg
840 60
841 tccagggttc cgaggagtat cgtcacgtgt attgcggtct tgttggagat tcctcagttg
842 120
843 tgcatgtaga tataaactta gtttagtcca cgatcggttt ctaatcgtgg atttttgtgg
844 180
```

Handwritten annotations: "see item #11 on error summary sheet.", "pls insert", "W-->", "E-->", "See item #1 on error summary sheet.", "Same error", "Same error"

RAW SEQUENCE LISTING   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:08:00

Input Set: E:\05-06-06 1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

```
E--> 845 gtttcggtcg ttgagcaaga attttgtgaa ttttttgtat tgggggaagg aaatggggtt
     846 240
E--> 847 atggcgatat cgttttcgtt gggttcaacg tgatcggtga gctccaggaa gggctggtca
     848 300
E--> 849 cttcacaatcc ggtattcgtc tcatcgagac gcatttatcg gttcattata tgtatatata
     850 360
E--> 851 tatatatata tatatgcaga gtcgattgtg ttgcaatttc tgaactaggt actgttgaat
     852 420
E--> 853 tgtagattgc cttcaagtag ctctcgatgt tggaatgacg gacacaaatt ctgctactga
     854 480
E--> 855 atgagaccat attctgcacc gttaattggt tttatgaata tatggtgtcg aattacattc
     856 540
E--> 857 cgtctcgaat ccatgcgccc tttctgcacg aacgttggtt tgtagttgta gtgcagccag
     858 600
E--> 859 tgtgtttggt ttaggattat gctttgacga tcgatgagtc cgtttcatgg ttttatactt
     860 660
E--> 861 gtcatttatc ttcttgtgat tttttgttta caaatgttcc cccaattgta acgtgggact
     862 720
E--> 863 tccgtgtgtg gtggttgctc aaattgatag ttttggtcat ttgatttgcg gagagcaatc
     864 780
E--> 865 ggtgtcatgg aaaatccctt cgactgcttt gatccaatca aagttctgct tgagccaatg
     866 840
E--> 867 tgagaggtgg aggattgggc ttcttctaag tgagaattct cg
     868 882
```

(handwritten) Same errors

(handwritten, in circle) The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VARIABLE LOCATION SUMMARY   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:08:01

Input Set: E:\05-06-06 1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

Error Explanation! ⟩

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

```
Seq#:3;  N Pos. 3,6,9,12,15,18
Seq#:4;  N Pos. 9,12,15,19,22,25
Seq#:5;  N Pos. 9,13
Seq#:6;  N Pos. 21
Seq#:31; N Pos. 6
Seq#:32; N Pos. 3,6,9,12,15
Seq#:33; N Pos. 3,6,9
Seq#:55; N Pos. 9,18
Seq#:56; N Pos. 3,6,15
Seq#:57; N Pos. 3,6,15,21
```

VERIFICATION SUMMARY   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:08:01

Input Set : E:\05-06-06-1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

```
L:9  M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:20 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:20 M:283 W: Missing Blank Line separator, <400> field identifier
L:21 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:1
L:28 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:29 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:30 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:2
L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:38 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:38 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3
L:39 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3
L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:39 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:3
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:47 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:47 M:283 W: Missing Blank Line separator, <400> field identifier
L:48 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4
L:48 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:4
L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:56 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:56 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:57 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:5
L:64 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:65 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6
L:65 M:283 W: Missing Blank Line separator, <400> field identifier
L:66 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6
L:66 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:66 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:6
L:73 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:74 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:74 M:283 W: Missing Blank Line separator, <400> field identifier
L:75 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:7
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:83 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
L:83 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:8
L:91 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:92 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
```

VERIFICATION SUMMARY   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:08:01

Input Set: E:\05-06-06-1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

```
L:92 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:9
L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:101 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:10
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:110 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:110 M:283 W: Missing Blank Line separator, <400> field identifier
L:111 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:11
L:118 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:119 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12
L:119 M:283 W: Missing Blank Line separator, <400> field identifier
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:127 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:128 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:129 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:13
L:136 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:137 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:138 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:14
L:145 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:146 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:146 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:15
L:154 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:155 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:155 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:16
L:163 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:164 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:164 M:283 W: Missing Blank Line separator, <400> field identifier
L:165 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:17
L:172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:173 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:18
L:173 M:283 W: Missing Blank Line separator, <400> field identifier
L:174 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:18
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:182 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:19
L:182 M:283 W: Missing Blank Line separator, <400> field identifier
L:183 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:19
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:191 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:20
L:191 M:283 W: Missing Blank Line separator, <400> field identifier
L:192 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:20
L:199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:200 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:21
L:200 M:283 W: Missing Blank Line separator, <400> field identifier
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/539,725

DATE: 06/29/2005
TIME: 14:08:01

Input Set : E:\05-06-06 1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

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L:201 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:21
L:208 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:209 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:22
L:209 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:22
L:217 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:218 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:23
L:218 M:283 W: Missing Blank Line separator, <400> field identifier
L:219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:23
L:226 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:227 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:24
L:227 M:283 W: Missing Blank Line separator, <400> field identifier
L:228 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:24
L:235 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:236 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25
L:236 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:25
L:244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:245 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26
L:245 M:283 W: Missing Blank Line separator, <400> field identifier
L:246 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:26
L:253 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:254 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27
L:254 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:27
L:262 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:263 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:28
L:263 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:28
L:271 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:272 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29
L:272 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:29
L:280 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:281 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:30
L:281 M:283 W: Missing Blank Line separator, <400> field identifier
L:282 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:30
L:289 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
L:290 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31
L:290 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:31
L:291 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:31
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:291 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:31
L:298 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:299 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:32
L:299 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:32
L:300 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:32
```

VERIFICATION SUMMARY   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:08:01

Input Set: E:\05-06-06-1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

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L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:300 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:32
L:307 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:308 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:33
L:308 M:283 W: Missing Blank Line separator, <400> field identifier
L:309 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:33
L:309 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:33
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:309 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:33
L:316 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:317 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:34
L:317 M:283 W: Missing Blank Line separator, <400> field identifier
L:318 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:34
L:325 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:326 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:35
L:326 M:283 W: Missing Blank Line separator, <400> field identifier
L:327 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:35
L:334 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:335 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:36
L:335 M:283 W: Missing Blank Line separator, <400> field identifier
L:336 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:36
L:344 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:37
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:345 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:37
L:353 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:38
L:353 M:283 W: Missing Blank Line separator, <400> field identifier
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:38
L:362 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:39
L:362 M:283 W: Missing Blank Line separator, <400> field identifier
L:363 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:39
L:371 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:40
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:372 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:40
L:380 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:41
L:380 M:283 W: Missing Blank Line separator, <400> field identifier
L:381 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:41
L:389 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:42
L:389 M:283 W: Missing Blank Line separator, <400> field identifier
L:390 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:42
L:398 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:43
L:398 M:283 W: Missing Blank Line separator, <400> field identifier
L:399 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:43
L:407 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:44
L:407 M:283 W: Missing Blank Line separator, <400> field identifier
L:408 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:44
L:416 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:45
L:416 M:283 W: Missing Blank Line separator, <400> field identifier
L:417 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:45
L:425 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46
```

VERIFICATION SUMMARY   DATE: 06/29/2005
PATENT APPLICATION: US/10/539,725   TIME: 14:08:01

Input Set : E:\05-06-06 1041WO.txt
Output Set: N:\CRF4\06292005\J539725.raw

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L:425 M:283 W: Missing Blank Line separator, <400> field identifier
L:426 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:46
L:434 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:47
L:434 M:283 W: Missing Blank Line separator, <400> field identifier
L:435 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:47
L:443 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:48
L:443 M:283 W: Missing Blank Line separator, <400> field identifier
L:444 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:48
L:452 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:49
L:452 M:283 W: Missing Blank Line separator, <400> field identifier
L:453 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:49
L:461 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:50
L:461 M:283 W: Missing Blank Line separator, <400> field identifier
L:462 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:50
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
```